Novel Fold and Capsid-binding Properties of the Lambda-phage Display Platform Protein gpD

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Abstract No. yang2125
Beamline(s): **X9B**

The crystal structure of gpD, the capsid-stabilizing protein of bacteriophage λ, was solved at 1.1 Å resolution. Data were obtained from pseudo-merohedrally twinned crystals in space group $P2_1$ and refined with anisotropic temperature factors to an R of 0.098 (R_{free} = 0.132). GpD comprises 109 residues and has a novel fold with an unusually low content of regular secondary structure. Non-crystallographic trimers with substantial inter-subunit interfaces were observed. The C-termini are well ordered and located on one side of the trimer, relatively far from its local three-fold axis. The N-termini are disordered up to Ser15, which is close to the three-fold axis and on the same side as the C-termini. A density map of the icosahedral viral capsid at 15 Å resolution, obtained by cryo-electron microscopy and image reconstruction, reveals gpD trimers, seemingly indistinguishable from the ones seen in the crystals, at all 3-fold sites. The map further reveals that the side of the trimer that binds to the capsid is the side on which both termini reside. Despite this orientation of the gpD trimer, fusion proteins connected by linker peptides to either terminus bind to the capsid, allowing protein and peptide display.